

Supplemental material

Wang et al., <https://doi.org/10.1083/jcb.201901155>

Provided online are nine tables in a PDF. Table S1 lists the yeast strains used in this study. Table S2 lists the plasmids used in this study. Table S3 lists the reaction formulae used in the standard computational model. Table S4 lists the reaction formulae used in the monomeric-receptor variation of the computational model. Table S5 lists the equations corresponding to Fig. S3. Table S6 lists the reaction-diffusion equations used in the computational model. Table S7 lists the equations that describe the local delivery rates of receptor dimers and heterotrimeric G proteins in the computational model. Table S8 lists the variables and parameters used in the computational model. Table S9 shows the sensitivity of model performance to the most critical unpublished parameters.

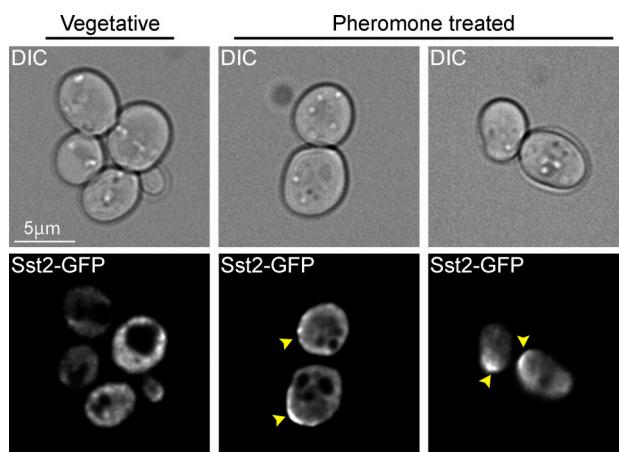


Figure S1. Pheromone induces translocation of Sst2-GFP from the cytoplasm to the PM. MAT α cells expressing Sst2 tagged with GFP in situ were imaged before and 60 min after isotropic pheromone treatment. Representative DIC and fluorescent images are shown. The arrowheads indicate the Sst2-GFP signal on the PM.

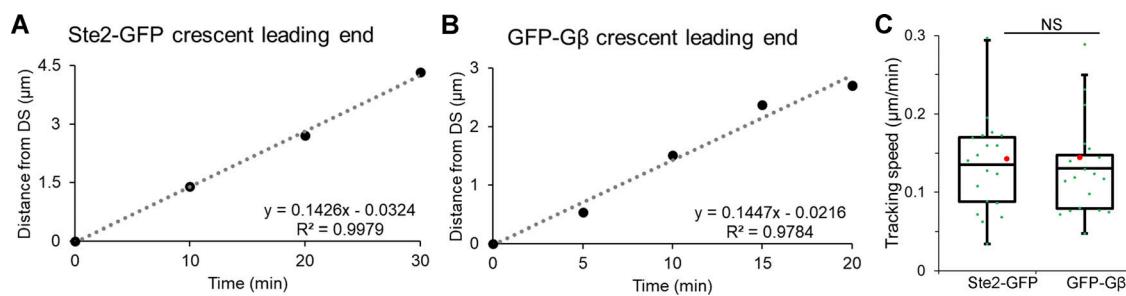


Figure S2. Ste2-GFP and GFP-G β tracking rates. Fluorescent intensities of Ste2-GFP and GFP-G β in MAT α cells that formed zygotes were quantified with ImageJ. Polarized crescents were defined as comprising the pixels with values $\geq 20\%$ greater than the mean signal intensity of the PM. Tracking rates were determined by plotting the position of each crescent's leading edge as a function of time and taking the slopes of the lines resulting from linear regression. **(A)** Representative plot and linear regression of Ste2-GFP during tracking. **(B)** Representative plot and linear regression of GFP-G β during tracking. **(C)** Box scatterplots showing the mean tracking rates of the receptor and G β reporters. Ste2-GFP = 0.135 ± 0.013 and GFP-G β = 0.130 ± 0.013 $\mu\text{m}/\text{min} \pm \text{SEM}$; $n = 20$ for each (two trials); $P > 0.80$. The red dots indicate the tracking rates of the cells represented in A and B.

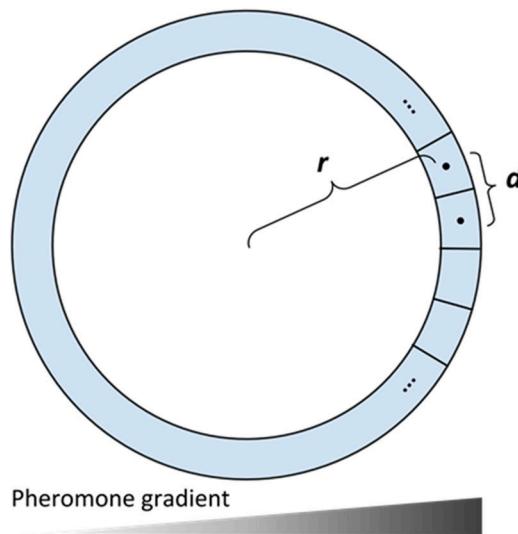


Figure S3. **Spatial model of the yeast PM.** r , cell radius; d , surface distance between neighboring wedges given by Eq. 1 in Table S5.

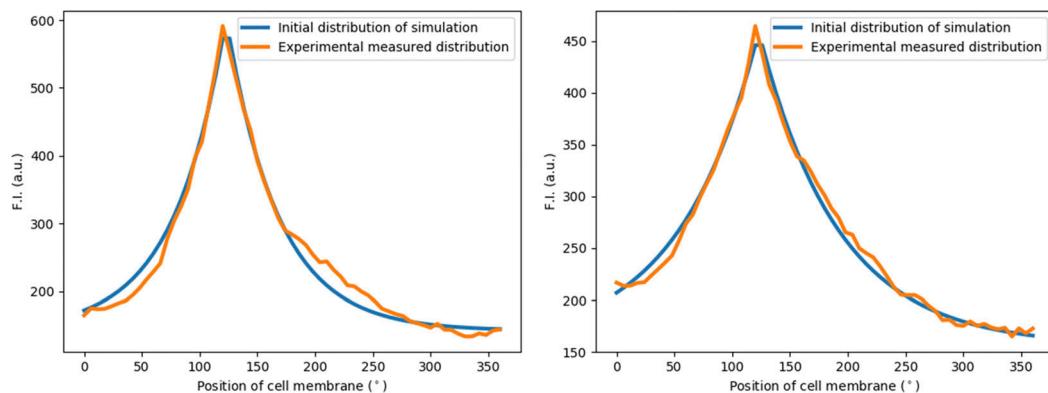


Figure S4. **The initial distributions of inactive receptor dimers and heterotrimeric G proteins in the standard computational model compared with the experimentally determined distributions of the receptor and G β taken from Fig. 2 (Start).** The experimentally determined plots represent the normalized and averaged distributions of the receptor (left) and G β (right). $n = 20$ for each reporter.

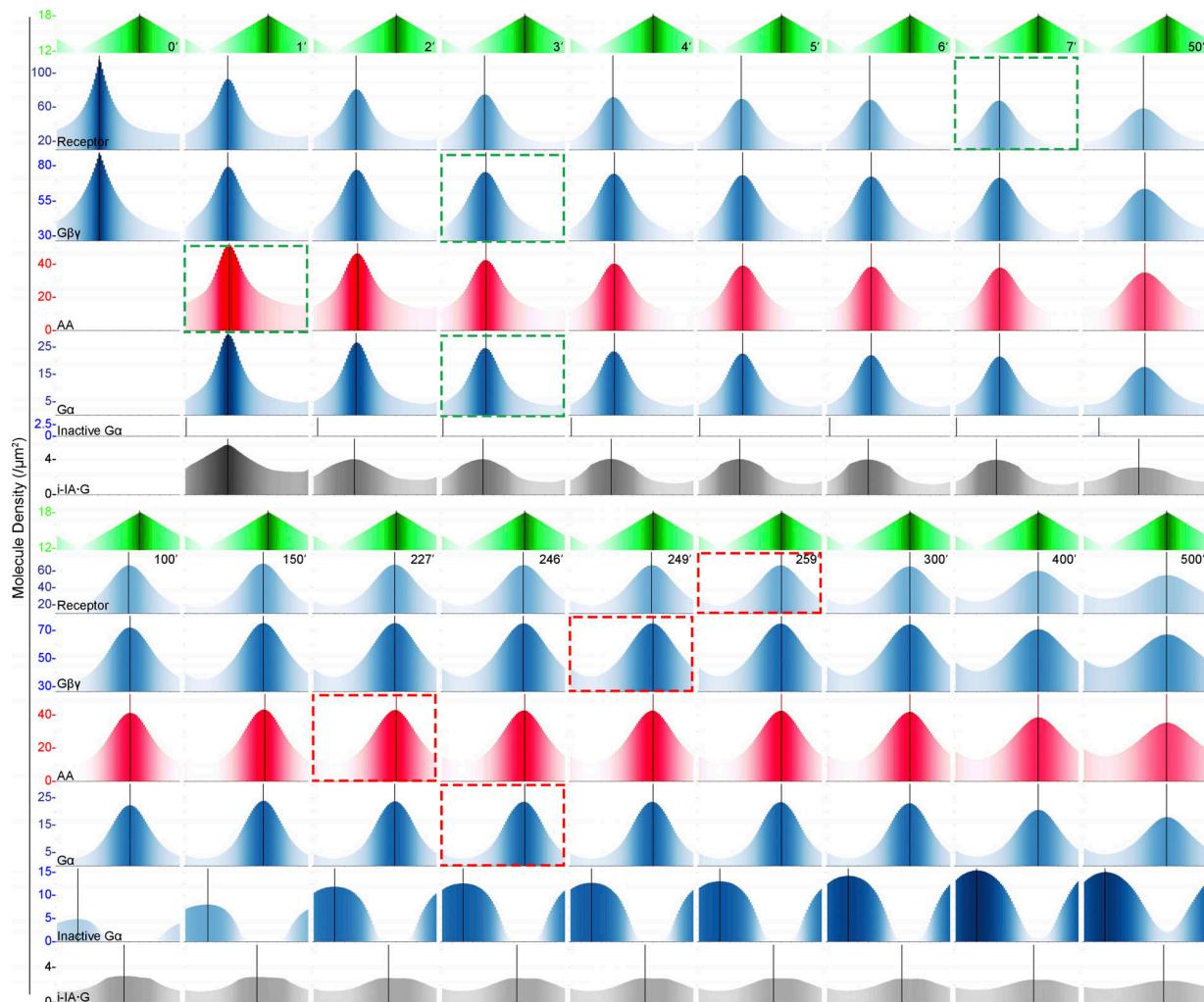
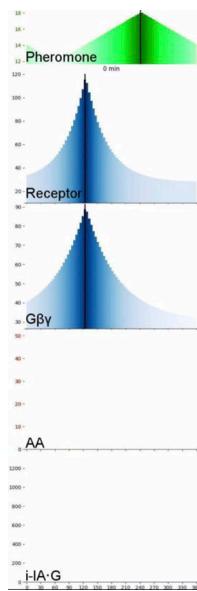
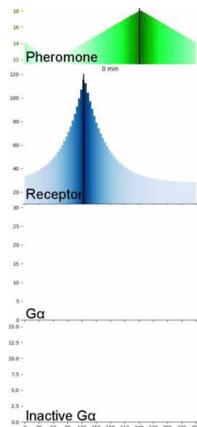


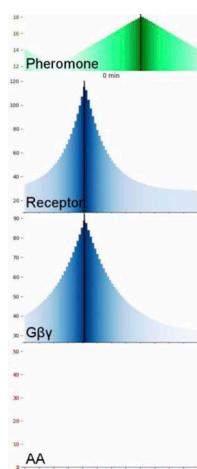
Figure S5. Outputs of the key parameters that underlie tracking in the standard model. The x axis of each plot corresponds to the cell circumference. Vertical black lines indicate the peak values of each parameter at each time point. The green panels show the applied pheromone gradient. The dashed green and red boxes indicate the start and end of tracking, respectively. Total receptor, total $\text{G}\beta\gamma$, AA receptor dimer (AA), active $\text{G}\alpha$, inactive $\text{G}\alpha$, and the cumulative internalization of IA-receptor dimer bound to one heterotrimeric G protein (i-IA-G) are shown from top to bottom. F.I., fluorescence intensity.



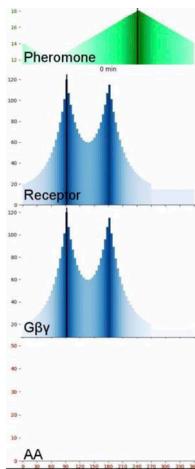
Video 1. Animation of receptor, $G\beta\gamma$, AA, and i-IA-G outputs from the standard model. The x axis of each plot corresponds to the cell circumference. Vertical black lines indicate the peak values of each parameter at each time point. The green panel (top) shows the applied pheromone gradient. Total receptor, total $G\beta\gamma$, AA receptor dimer (AA), and the cumulative internalization of IA-receptor dimer bound to one heterotrimeric G protein (i-IA-G) are shown from top to bottom. The distributions of parameter levels around the cell circumference are shown in 1-min intervals for 500 min.



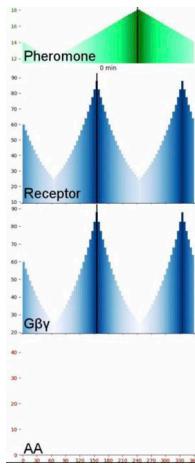
Video 2. Animation of receptor, $G\alpha$, and inactive $G\alpha$ outputs from the standard model. The x axis of each plot corresponds to the cell circumference. Vertical black lines indicate the peak values of each parameter at each time point. The green panel (top) shows the applied pheromone gradient. Total receptor, active $G\alpha$, and inactive $G\alpha$ are shown from top to bottom. The distributions of parameter levels around the cell circumference are shown in 1-min intervals for 500 min.



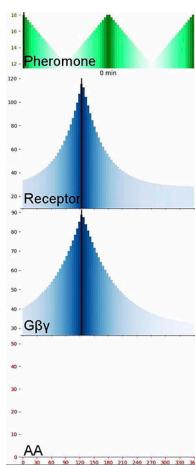
Video 3. Animation of representative outputs from the reorientation simulation. The x axis of each plot corresponds to the cell circumference. Vertical black lines indicate the peak values of each parameter at each time point. The green panel (top) shows the applied pheromone gradient. The pheromone gradient was rotated 90° at 201 min. Total receptor, total $G\beta\gamma$, and AA receptor dimer (AA) are shown from top to bottom. The distributions of parameter levels around the cell circumference are shown in 1-min intervals for 500 min.



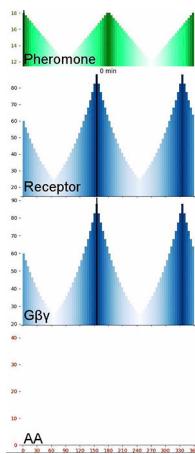
Video 4. Animation of representative outputs from the modified model with two initial polarity sites on the same side of the cell relative to the gradient source. The x axis of each plot corresponds to the cell circumference. Vertical black lines indicate the peak values of each parameter at each time point. The green panel (top) shows the applied pheromone gradient. Total receptor, total G $\beta\gamma$, and AA receptor dimer (AA) are shown from top to bottom. The distributions of parameter levels around the cell circumference are shown in 1-min intervals for 280 min.



Video 5. Animation of representative outputs from the modified model with two initial polarity sites on opposite sides of the cell relative to the gradient source. The x axis of each plot corresponds to the cell circumference. Vertical black lines indicate the peak values of each parameter at each time point. The green panel (top) shows the applied pheromone gradient. Total receptor, total G $\beta\gamma$, and AA receptor dimer (AA) are shown from top to bottom. The distributions of parameter levels around the cell circumference are shown in 1-min intervals for 280 min.



Video 6. Animation of representative outputs from the standard model challenged by two equal gradients. The x axis of each plot corresponds to the cell circumference. Vertical black lines indicate the peak values of each parameter at each time point. The green panel (top) shows the applied pheromone gradient. Total receptor, total G $\beta\gamma$, and AA receptor dimer (AA) are shown from top to bottom. The distributions of parameter levels around the cell circumference are shown in 1-min intervals for 150 min.



Video 7. Animation of representative outputs from a modified model with two initial polarity sites challenged by two equal gradient sources. The x axis of each plot corresponds to the cell circumference. Vertical black lines indicate the peak values of each parameter at each time point. The green panel (top) shows the applied pheromone gradient. Total receptor, total G $\beta\gamma$, and AA receptor dimer (AA) are shown from top to bottom. The distributions of parameter levels around the cell circumference are shown in 1-min intervals for 200 min.